1

SEQUENCE LISTING

<110>  Proteome Systems Intellectual Propoerty Pty Ltd

5  <120>  Method of isolating a protein

<130>  502469/PXM

<160>  26
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<170>  PatentIn version 3.1

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    Ala Val Asp Ser Pro Ile Glu Asp Thr Pro Ile Ile Arg Asn Gly Gly
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    Glu Leu Thr Asn Leu Leu Gly Asn Ser Glu Thr Thr Leu Ala Leu Arg
         50                  55                  60

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    Asn Glu Glu Ser Ala Thr Ala Asp Leu Thr Ala Ala Ala Val Ala Asp
    65                  70                  75                  80


40  Thr Val Ala Ala Ala Ala Ala Glu Asn Ala Gly Ala Ala Ala Trp Glu
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    Ala Ala Ala Ala Ala Asp Ala Leu Ala Lys Ala Lys Ala Asp Ala Leu
45               100                 105                 110


    Lys Glu Phe Asn Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile
             115                 120                 125
50
    Asn Asn Ala Lys Thr Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val
             130                 135                 140
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    Val Glu Ser Ala Lys Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu
    145                 150                 155                 160


60  Ser Asp Phe Leu Lys Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser
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    Ile Glu Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys

2

|   | 180 | | | | | 185 | | | | | 190 | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

5   Tyr Gly Val Ser Asp Tyr His Lys Asn Leu Ile Asn Asn Ala Lys Thr
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    Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val Val Glu Ser Ala Lys
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    Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu Ser Asp Phe Leu Lys
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    Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser Ile Glu Leu Ala Glu
            245          250           255

20  Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp
            260          265          270

25  Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys
        275          280         285

    Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Lys Thr Asp Thr Tyr
        290          295          300
30

    Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu
    305            310          315          320
35

    Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn
            325          330          335

40  Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr
            340          345          350

    Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr
45         355          360         365

    Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys
        370          375          380
50

    Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
    385            390          395          400
55

    Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
            405          410          415

60  Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
            420          425          430

    Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile

              435                    440                    445

     Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
5        450                 455             460

     Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
     465             470             475                 480
10

     Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
                 485             490                 495
15

     Glu Met Val Thr Glu Val Pro Gly Asp Ala Pro Thr Glu Pro Glu Lys
             500             505             510

20   Pro Glu Ala Ser Ile Pro Leu Val Pro Leu Thr Pro Ala Thr Pro Ile
             515             520             525

     Ala Lys Asp Asp Ala Lys Lys Asp Asp Thr Lys Lys Glu Asp Ala Lys
25       530             535             540

     Lys Pro Glu Ala Lys Lys Glu Asp Ala Lys Lys Ala Glu Thr Leu Pro
     545             550             555             560
30

     Thr Thr Gly Glu Gly Ser Asn Pro Phe Phe Thr Ala Ala Ala Leu Ala
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                 20              25                  30

     Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro Ala Ala Asn Ala
. 60         35              40                  45

     Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
         50              55                  60

4

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    Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
    65              70              75              80
5

    Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
                85              90              95
10
    Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Lys Phe
                100             105             110

15  Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
                115             120             125

    Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp
20      130             135             140

    Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
    145             150             155             160
25
    Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn
                165             170             175
30
    Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
                180             185             190

35  Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
                195             200             205

    Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala
40      210             215             220

    Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
    225             230             235             240
45
    His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
                245             250             255
50
    Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys
                260             265             270

55  Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro
                275             280             285

    Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
60      290             295             300

    Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
    305             310             315             320
```

5

```
    Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
 5                  325             330             335

    Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
                    340             345             350
10
    Gly Lys Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly Asp Thr
                    355             360             365

15  Val Asn Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile Ala
                    370             375             380

    Val Asp Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly Gln Glu
20  385                 390             395             400

    Leu Val Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala Asn Lys
                    405             410             415
25
    Ala Gln Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile Gly Thr
                    420             425             430
30
    Thr Val Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu Leu Ala
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35  Gly Arg Arg Arg Glu Leu
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    1               5               10              15

50  Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
                    20              25              30

    Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
55                  35              40              45

    Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
                    50              55              60
60
    Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
        65              70              75              80
```

6

```
        Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
                        85              90              95

  5
        Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
                    100             105             110

 10     Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
                    115             120             125

 15     Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
            130             135             140

        Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
        145             150             155             160
 20
        Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
                    165             170             175

 25
        Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
                    180             185             190

 30     Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu
                    195             200             205

 35     Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp
            210             215             220

        Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn
        225             230             235             240
 40
        Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu
                    245             250             255

 45
        Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr
                    260             265             270

 50     Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg
                    275             280             285

 55     Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val
            290             295             300

        Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
        305             310             315             320
 60
        Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
                    325             330             335
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7

```
        Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala
                    340             345             350
 5
        Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu
                355             360             365

10      Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn
                370             375             380

        Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Lys Glu
15      385             390             395             400

        Gln Val Thr Ile Lys Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln
20                      405             410             415

        Thr Ala Thr Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr
                    420             425             430
25
        Arg Tyr Ala Asp Leu Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp
                435             440             445

30      Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly Lys Glu
            450             455             460

        Glu Pro Glu Glu Thr Pro Glu Lys Pro Glu Val Gln Asp Gly Tyr Ala
35      465             470             475             480

        Ser Tyr Glu Glu Ala Glu Ala Ala Lys Glu Ala Leu Lys Asn Asp
40                  485             490             495

        Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr
                    500             505             510
45
        Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Glu Lys Pro Glu Ala
                515             520             525

50      Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Ala Lys Lys
                530             535             540

55      Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly
        545             550             555             560

        Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr
60                  565             570             575

        Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
                    580             585             590
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      Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
              595             600             605
 5
      Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr
              610             615             620
10    Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu
      625             630             635             640
15    Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
                      645             650             655
      Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
                  660             665             670
20
      Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu
              675             680             685
25
      Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser
          690             695             700
30    Leu Ser Ser Val Ala Gly Ala Phe Ile Ser Leu Lys Lys Arg Lys
      705             710             715
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      <213>   protein A mimetic

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45    Glu Glu Gln Arg
                      20
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50    <210>   5
      <211>   16
      <212>   PRT
      <213>   protein A mimetic

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      1               5               10              15
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Phe Arg


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Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys
1               5                   10                  15


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<400>  8

Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys
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<400>  9

Val Val Gly His Gly Gln Asn Ile Arg
1               5


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<213>  fragment of M. tuberculosis glutamine synthetase

<400>  10

Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
1               5                   10                  15

Leu Val Arg


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<400>  11

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1               5                   10                  15


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<213>   M. tuberculosis glutamine synthetase

<400>   12

Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg
1       .        5                   10                  15


Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
            20                  25                  30


Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
        35                  40                  45


Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
        50                  55                  60


Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
65                  70                  75                  80


Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
                85                  90                  95


Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
            100                 105                 110


Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
            115                 120                 125


Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
        130                 135                 140


Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
145                 150                 155                 160


Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
                165                 170                 175


Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
    .           180             .       185                 190


Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
        195                 200                 205
```

11

```
     Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
         210             215             220

 5   Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
         225             230             235             240

10   Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
                 245             250             255

     Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
15           260             265             270

     Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
20           275             280             285

     Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
25       290             295             300

     Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
     305             310             315             320

30   Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
                 325             330             335

     Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
35           340             345             350

     Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
40       355             360             365

     Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
         370             375             380

45   Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
     385             390             395             400

50   Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
                 405             410             415

     Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
55           420             425             430

     Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
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60   Glu Arg Ile Arg Gly Phe Glu Arg Leu
         450             455
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12

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<222>  (1)..(1191)
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Val Ala Lys Ala Lys Phe Gln Arg Thr Lys Pro His Val Asn Ile Gly
1               5                  10                  15

acc atc ggt cac gtt gac cac ggc aag acc acc ctg acc gcg gct atc     96
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
                20                  25                  30

acc aag gtc ctg cac gac aaa ttc ccc gat ctg aac gag acg aag gca    144
Thr Lys Val Leu His Asp Lys Phe Pro Asp Leu Asn Glu Thr Lys Ala
            35                  40                  45

ttc gac cag atc gac aac gcc ccc gag gag cgt cag cgc ggt atc acc    192
Phe Asp Gln Ile Asp Asn Ala Pro Glu Glu Arg Gln Arg Gly Ile Thr
        50                  55                  60

atc aac atc gcg cac gtg gag tac cag acc gac aag cgg cac tac gca    240
Ile Asn Ile Ala His Val Glu Tyr Gln Thr Asp Lys Arg His Tyr Ala
65                  70                  75                  80

cac gtc gac gcc cct ggc cac gcc gac tac atc aag aac atg atc acc    288
His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr
                85                  90                  95

ggc gcc gcg cag atg gac ggt gcg atc ctg gtg gtc gcc gcc acc gac    336
Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp
                100                 105                 110

ggc ccg atg ccc cag acc cgc gag cac gtt ctg ctg gcg cgt caa gtg    384
Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val
            115                 120                 125

ggt gtg ccc tac atc ctg gta gcg ctg aac aag gcc gac gca gtg gac    432
Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Ala Asp Ala Val Asp
        130                 135                 140

gac gag gag ctg ctc gaa ctc gtc gag atg gag gtc cgc gag ctg ctg    480
Asp Glu Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu
145                 150                 155                 160

gct gcc cag gaa ttc gac gag gac gcc ccg gtt gtg cgg gtc tcg gcg    528
Ala Ala Gln Glu Phe Asp Glu Asp Ala Pro Val Val Arg Val Ser Ala
                165                 170                 175

ctc aag gcg ctc gag ggt gac gcg aag tgg gtt gcc tct gtc gag gaa    576
Leu Lys Ala Leu Glu Gly Asp Ala Lys Trp Val Ala Ser Val Glu Glu
            180                 185                 190

ctg atg aac gcg gtc gac gag tcg att ccg gac ccg gtc cgc gag acc    624
Leu Met Asn Ala Val Asp Glu Ser Ile Pro Asp Pro Val Arg Glu Thr
            195                 200                 205

gac aag ccg ttc ctg atg ccg gtc gag gac gtc ttc acc att acc ggc    672
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13

```
      Asp Lys Pro Phe Leu Met Pro Val Glu Asp Val Phe Thr Ile Thr Gly
          210             215             220

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      Arg Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Val Ile Asn Val
          225             230             235             240

10    aac gag gaa gtt gag atc gtc ggc att cgc cca tcg acc acc aag acc       768
      Asn Glu Glu Val Glu Ile Val Gly Ile Arg Pro Ser Thr Thr Lys Thr
                          245             250             255

      acc gtc acc ggt gtg gag atg ttc cgc aag ctg ctc gac cag ggc cag       816
      Thr Val Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Gln Gly Gln
                      260             265             270
15
      gcg ggc gac aac gtt ggt ttg ctg ctg cgg ggc gtc aag cgc gag gac       864
      Ala Gly Asp Asn Val Gly Leu Leu Leu Arg Gly Val Lys Arg Glu Asp
                  275             280             285

20    gtc gag cgt ggc cag gtt gtc acc aag ccc ggc acc acc acg ccg cac       912
      Val Glu Arg Gly Gln Val Val Thr Lys Pro Gly Thr Thr Thr Pro His
          290             295             300

25    acc gag ttc gaa ggc cag gtc tac atc ctg tcc aag gac gag ggc ggc       960
      Thr Glu Phe Glu Gly Gln Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly
      305             310             315             320

      cgg cac acg ccg ttc ttc aac aac tac cgt ccg cag ttc tac ttc cgc      1008
      Arg His Thr Pro Phe Phe Asn Asn Tyr Arg Pro Gln Phe Tyr Phe Arg
30                    325             330             335

      acc acc gac gtg acc ggt gtg gtg aca ctg ccg gag ggc acc gag atg      1056
      Thr Thr Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Thr Glu Met
                      340             345             350
35
      gtg atg ccc ggt gac aac acc aac atc tcg gtg aag ttg atc cag ccc      1104
      Val Met Pro Gly Asp Asn Thr Asn Ile Ser Val Lys Leu Ile Gln Pro
                  355             360             365

40    gtc gcc atg gac gaa ggt ctg cgt ttc gcg atc cgc gag ggt ggc cgc      1152
      Val Ala Met Asp Glu Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg
          370             375             380

45    acc gtg ggc gcc ggc cgg gtc acc aag atc atc aag tag                  1191
      Thr Val Gly Ala Gly Arg Val Thr Lys Ile Ile Lys
      385             390             395
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50    <210>   14
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      <212>   PRT
      <213>   M. tuberculosis Elongation Factor TU

55    <400>   14

      Val Ala Lys Ala Lys Phe Gln Arg Thr Lys Pro His Val Asn Ile Gly
      1               5               10              15

60    Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
                      20              25              30


      Thr Lys Val Leu His Asp Lys Phe Pro Asp Leu Asn Glu Thr Lys Ala
```

14

```
              35                      40                      45

5    Phe Asp Gln Ile Asp Asn Ala Pro Glu Glu Arg Gln Arg Gly Ile Thr
         50                  55                  60

     Ile Asn Ile Ala His Val Glu Tyr Gln Thr Asp Lys Arg His Tyr Ala
10       65                  70                  75                  80

     His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr
                     85                  90                  95
15
     Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp
                     100                 105                 110

20   Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val
                 115                 120                 125

     Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Ala Asp Ala Val Asp
25               130                 135                 140

     Asp Glu Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu
         145                 150                 155                 160
30
     Ala Ala Gln Glu Phe Asp Glu Asp Ala Pro Val Val Arg Val Ser Ala
                     165                 170                 175
35
     Leu Lys Ala Leu Glu Gly Asp Ala Lys Trp Val Ala Ser Val Glu Glu
                     180                 185                 190

40   Leu Met Asn Ala Val Asp Glu Ser Ile Pro Asp Pro Val Arg Glu Thr
                 195                 200                 205

     Asp Lys Pro Phe Leu Met Pro Val Glu Asp Val Phe Thr Ile Thr Gly
45       210             215                 220

     Arg Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Val Ile Asn Val
50       225             230                 235                 240

     Asn Glu Glu Val Glu Ile Val Gly Ile Arg Pro Ser Thr Thr Lys Thr
                     245                 250                 255
55
     Thr Val Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Gln Gly Gln
                 260                 265                 270

60   Ala Gly Asp Asn Val Gly Leu Leu Leu Arg Gly Val Lys Arg Glu Asp
             275                 280                 285

     Val Glu Arg Gly Gln Val Val Thr Lys Pro Gly Thr Thr Thr Pro His
```

15

```
              290                  295                  300

   Thr Glu Phe Glu Gly Gln Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly
 5 305                  310              315             320

   Arg His Thr Pro Phe Phe Asn Asn Tyr Arg Pro Gln Phe Tyr Phe Arg
10                  325              330              335

   Thr Thr Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Thr Glu Met
                   340              345              350
15
   Val Met Pro Gly Asp Asn Thr Asn Ile Ser Val Lys Leu Ile Gln Pro
                   355              360              365

20 Val Ala Met Asp Glu Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg
       370              375              380

   Thr Val Gly Ala Gly Arg Val Thr Lys Ile Ile Lys
25 385              390              395


   <210>  15
   <211>  17
30 <212>  PRT
   <213>  fragment of M. tuberculosis Elongation factor TU

   <400>  15

35 Lys Leu Leu Asp Gln Gly Gln Ala Gly Asp Asn Val Gly Leu Leu Leu
   1              5              10              15


   Arg
40


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   <400>  16

50 Leu Arg Pro Leu His Asp Arg
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Met Lys Leu Arg Pro Leu His Asp Arg
1               5


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Met Lys Leu Arg Pro Leu His Asp Arg
1               5


<210>   20
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<400>   20

Val Val Phe Gly Pro Tyr Ser Gly Ser Asn Ala Ile Lys
1               5                   10


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<400>   21

Leu Arg Pro Leu His Asp Arg Val Val Ile Arg
1               5                   10


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<400>   22

Val Leu Asp Asn Gly Glu Val Arg Ala Leu Ala Val Lys
1               5                   10


<210>   23
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<400>   23

Thr Ala Gly Gly Ile Val Leu Pro Gly Ser Ala Ala Glu Lys Pro Asn
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    Arg

5

    <210>  24
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10  <213>  fragment of P. aeruginosa GroES

    <400>  24

15  Val Gly Asp Lys Val Val Phe Gly Pro Tyr Ser Gly Ser Asn Ala Ile
    1               5                   10                  15


    Lys

20

    <210>  25
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25  <213>  P. aeruginosa GroES

    <400>  25

30  Met Lys Leu Arg Pro Leu His Asp Arg Val Val Ile Arg Arg Ser Glu
    1               5                   10                  15


    Glu Glu Thr Lys Thr Ala Gly Gly Ile Val Leu Pro Gly Ser Ala Ala
35                  20                  25                  30


    Glu Lys Pro Asn Arg Gly Glu Val Val Ala Val Gly Thr Gly Arg Val
                35                  40                  45
40
    Leu Asp Asn Gly Glu Val Arg Ala Leu Ala Val Lys Val Gly Asp Lys
                50                  55                  60


45  Val Val Phe Gly Pro Tyr Ser Gly Ser Asn Ala Ile Lys Val Asp Gly
    65                  70                  75                  80


    Glu Glu Leu Leu Val Met Gly Glu Ser Glu Ile Leu Ala Val Leu Glu
50                  85                  90                  95


    Asp

55

    <210>  26
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60  <213>  human Calgranulin B

    <400>  26

    Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile
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18

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      1                    5                   10                  15

  5   Asn Thr Phe His Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu
                  20                  25                  30

 10   Asn Gln Gly Glu Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe
              35                  40                  45

      Leu Lys Lys Glu Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu
          50                  55                  60
 15
      Asp Leu Asp Thr Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile
      65                  70                  75                  80

 20   Met Leu Met Ala Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu
                  85                  90                  95

 25   Gly Asp Glu Gly Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly
                  100                 105                 110

      Thr Pro

 30
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